

ON nucleic - nucleic search, using SW model

Run on:	January 7, 2004, 04:41:34	; Search time 23414 Seconds (without alignments)
		11736.119 Million cell updates/sec

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Searched: 2888711 seqs, 20454813386 residues

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Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 04 Maximum Match 1004 Listing first 43 summaries										
Database : General : 1: gb_ba.* 2: gb_hlg.* 3: gb_in.* 4: gb_ov.* 5: gb_ov.* 6: gb_pat.* 7: gb_ph.* 8: gb_ph.* 9: gb_ph.* 10: gb_ro.* 11: gb_ets.* 12: gb_ets.* 13: gb_vir.* 14: gb_vir.* 15: es_ba.* 16: es_ba.* 17: es_ba.* 18: es_in.* 19: es_in.* 20: es_on.* 21: es_or.* 22: es_or.* 23: es_pat.* 24: es_ph.* 25: es_ph.* 26: es_ph.* 27: es_ph.* 28: es_ph.* 29: es_ph.* 30: es_ph.* 31: es_ph.* 32: es_ph.* 33: es_ph.* 34: es_ph.* 35: es_ph.* 36: es_ph.* 37: es_ph.* 38: es_ph.* 39: es_ph.* 40: es_ph.* 41: es_ph.* 42: es_ph.* 43: es_ph.* 44: es_ph.* 45: es_ph.* 46: es_ph.* 47: es_ph.* 48: es_ph.* 49: es_ph.* 50: es_ph.* 51: es_ph.* 52: es_ph.* 53: es_ph.* 54: es_ph.* 55: es_ph.* 56: es_ph.* 57: es_ph.* 58: es_ph.* 59: es_ph.* 60: es_ph.* 61: es_ph.* 62: es_ph.* 63: es_ph.* 64: es_ph.* 65: es_ph.* 66: es_ph.* 67: es_ph.* 68: es_ph.* 69: es_ph.* 70: es_ph.* 71: es_ph.* 72: es_ph.* 73: es_ph.* 74: es_ph.* 75: es_ph.* 76: es_ph.* 77: es_ph.* 78: es_ph.* 79: es_ph.* 80: es_ph.* 81: es_ph.* 82: 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c 37 265 3.0 168076 AC021629 Homo sapi
38 265 3.0 168076 AC021629 Homo sapi
c 39 265 3.0 168076 AC021629 Homo sapi
40 264 3.0 168076 AC021629 Homo sapi
c 41 263.8 3.0 168076 AC021629 Homo sapi
42 263.8 3.0 168076 AC021629 Homo sapi
c 43 263.8 3.0 168076 AC021629 Homo sapi
44 263.8 3.0 168076 AC021629 Homo sapi
c 45 262.4 3.0 168076 AC021629 Homo sapi

```

```

Search completed: January 7, 2004, 17:54:50
Job time : 21475 secs

```

```

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```

```

OW nucleat - nucleic search, using nw model
Run on: January 7, 2004, 04:37:20 ; Search time 1564 Seconds
1593.410 Million cell updates/sec

Title: US-10-82-272-1
Perfect score: 6717
Sequence: 1593.410 Million cell updates/sec

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapex 1.0

Searched: 252756 seqs, 1349719017 residues 510512
Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum March 04
Maximum March 1004
Listing first 45 summaries

```

```

Database : N Consseq 1349017
1. /SID51/gcgdata/geneseq/geneseq-emb/NA1890.DAT.*
2. /SID51/gcgdata/geneseq/geneseq-emb/NA1891.DAT.*
3. /SID51/gcgdata/geneseq/geneseq-emb/NA1892.DAT.*
4. /SID51/gcgdata/geneseq/geneseq-emb/NA1893.DAT.*
5. /SID51/gcgdata/geneseq/geneseq-emb/NA1894.DAT.*
6. /SID51/gcgdata/geneseq/geneseq-emb/NA1895.DAT.*
7. /SID51/gcgdata/geneseq/geneseq-emb/NA1896.DAT.*
8. /SID51/gcgdata/geneseq/geneseq-emb/NA1897.DAT.*
9. /SID51/gcgdata/geneseq/geneseq-emb/NA1898.DAT.*
10. /SID51/gcgdata/geneseq/geneseq-emb/NA1899.DAT.*

```

```

11. /SID51/gcgdata/geneseq/geneseq-emb/NA1890.DAT.*
12. /SID51/gcgdata/geneseq/geneseq-emb/NA1891.DAT.*
13. /SID51/gcgdata/geneseq/geneseq-emb/NA1892.DAT.*
14. /SID51/gcgdata/geneseq/geneseq-emb/NA1893.DAT.*
15. /SID51/gcgdata/geneseq/geneseq-emb/NA1894.DAT.*
16. /SID51/gcgdata/geneseq/geneseq-emb/NA1895.DAT.*
17. /SID51/gcgdata/geneseq/geneseq-emb/NA1896.DAT.*
18. /SID51/gcgdata/geneseq/geneseq-emb/NA1897.DAT.*
19. /SID51/gcgdata/geneseq/geneseq-emb/NA1898.DAT.*
20. /SID51/gcgdata/geneseq/geneseq-emb/NA1899.DAT.*
21. /SID51/gcgdata/geneseq/geneseq-emb/NA2001.DAT.*
22. /SID51/gcgdata/geneseq/geneseq-emb/NA2002.DAT.*
23. /SID51/gcgdata/geneseq/geneseq-emb/NA2003.DAT.*
24. /SID51/gcgdata/geneseq/geneseq-emb/NA2004.DAT.*
25. /SID51/gcgdata/geneseq/geneseq-emb/NA2005.DAT.*

```

Fred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed.
 and is derived by analysis of the test score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	847	12.5	1113	24	AA070432	Novel human cDNA
	2	841	12.5	1113	24	AA070433	Novel human cDNA
	3	633.8	9.4	500	22	AA094043	Human neuroblaston
c	4	614.8	9.2	892	22	AA094044	Human neuroblaston
	5	385.2	5.7	710	22	AA023849	Human cDNA, accordin
	6	385.2	5.7	710	22	AA023849	Human cDNA, accordin
	7	268.4	4.0	2160	23	AB017451	Drosophila melanog
c	8	263	3.9	31405	22	AA067293	Human immune/haema
	9	263	3.9	31405	22	AA067293	Human immune/haema
	10	263	3.9	31405	22	AA067293	Human immune/haema
	11	259.6	3.9	138600	24	AB023161	Human cDNA, differe
	12	258.4	3.8	21332	22	AA074878	Human immune/haema
	13	258.4	3.8	21332	22	AA074878	Human immune/haema
	14	258.4	3.8	14286	22	AA083210	Human immune/haema
	15	258.2	3.8	14260	22	AA083183	Human immune/haema
	16	256.2	3.8	15610	22	AA016098	Human arionatriur
	17	256.2	3.8	15610	22	AA016098	Human arionatriur
c	18	253.3	3.8	32264	22	AA039420	Genomic sequence #
	19	253.2	3.8	32264	22	AA039420	Genomic sequence #
	20	253.2	3.8	32264	22	AA039420	Genomic sequence #
	21	253.2	3.8	32264	22	AA039420	Genomic sequence #
	22	253.2	3.8	32264	22	AA039420	Genomic sequence #
	23	253	3.8	21621	22	AA074867	Human immune/haema
	24	251.8	3.7	14260	22	AA083217	Human immune/haema
	25	251.8	3.7	14260	22	AA083217	Human immune/haema
	26	251.4	3.7	22482	22	AA073884	Human protease exp
	27	251.4	3.7	3712	23	AB029765	Human protease exp
c	28	250.8	3.7	3138	22	AA071948	Human immune/haema
	29	250.8	3.7	3138	22	AA071948	Human immune/haema
	30	250.4	3.7	36437	24	AB088613	Human cDNA, accordin
	31	250.2	3.7	126439	24	AB088177	Human osteoblast d
	32	250	3.7	15772	22	AA063220	Human immune/haema

c 33 250 3.7 1503841 24 AET00010 Human neurotrophin 1
 c 34 250 3.7 1503841 24 AET01003 Human neurotrophin 1
 c 35 250 3.7 1503841 24 AET01003 Human neurotrophin 1
 c 36 250 3.7 1503900 22 AKR6713 Human immunoglobulin
 c 37 249.6 3.7 6547 22 AKR83105 Human immunoglobulin
 c 38 249.6 3.7 6547 22 AKR83105 Human immunoglobulin
 c 39 249.6 3.7 6547 22 AKR83105 Human immunoglobulin
 c 40 249.4 3.7 27289 22 AKR34624 Human immunoglobulin
 c 41 249.2 3.7 231724 24 AKR08143 Human osteoblast d
 c 42 249 3.7 18488 22 AKR83173 Human immunoglobulin
 c 43 248.6 3.7 17424 24 AKR61222 Human immunoglobulin
 c 44 248.6 3.7 28123 24 AKR59441 Human multigene re

Search completed: January 7, 2004, 11:23:28
 Job time : 1581 secs

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ON nucleic - nucleic search, using sw model

Run on: January 7, 2004, 09:48:03 , Search time 12360 Seconds

13186.847 Million Cell Updates/sec

Title: US-10-02-272-1

Sequence: 1 GCGCGCGCTCCCGCGCA.....taaaataaaataaaataaa 6717

Scoring table: IDENTITY_BUC
 Gapop 15.0 , Gapext 1.0

Searched: 22781392 seqs, 12152218056 retdashes

Total number of hits satisfying chosen parameters: 45662784

Minimum DB seq length: 0

Maximum DB seq length: 200000900

Post-processing: Minimum Match 04

Maximum Match 1004

Listing first 45 summaries

Database : EST.*

- 1: em_sctba*
- 2: em_sctba*
- 3: em_sctba*
- 4: em_sctba*
- 5: em_sctba*
- 6: em_sctba*
- 7: em_sctba*
- 8: em_sctba*
- 9: SP_sct1*

- 10: SP_sct21*
- 11: SP_sct*
- 12: SP_sct*
- 13: SP_sct4*
- 14: SP_sct5*
- 15: em_sctfam*
- 16: em_sctfam*
- 17: em_sctfam*
- 18: em_sctfam*
- 19: em_sctfam*
- 20: em_sctfam*
- 21: em_sctfam*
- 22: em_sctfam*
- 23: em_sctfam*
- 24: em_sctfam*
- 25: em_sctfam*
- 26: em_sctfam*
- 27: em_sctfam*
- 28: em_sctfam*
- 29: SP_sct21*

Fred. No. is the number of results predicted by chance to have a
 significant difference between the two distributions being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	2	796.2	11.9	3487	11	AKR52155	AKR52155 Nus muscu
2	3	677	10.1	901	13	BQ21652	BQ21652 AGNCOURT
3	4	652.6	9.7	969	13	BX288215	BX288215 BX288215
4	5	615.2	9.3	1010	13	BX288215	BX288215 BX288215
5	6	515.2	7.7	536	2	HSN096259	HSN096259
6	7	472.2	7.0	477	9	A1936589	A1936589 w22g06.x
7	8	458	7.0	522	2	HSN02075	HSN02075
8	9	435.6	6.5	575	12	BH087995	BH087995 501340.MA
9	10	435.6	6.5	575	12	BH087995	BH087995 501340.MA
10	11	425	6.3	425	9	A1838884	A1838884 w66a05.x
11	12	411	6.1	411	9	AA503000	AA503000 CP95002.a
12	13	391.2	5.9	641	13	BH52125	BH52125
13	14	385	5.7	649	14	CB41644	CB41644 592147.MA
14	15	366	5.4	366	10	BS246007	BS246007 MS01a03.x
15	16	366	5.4	366	10	BS246007	BS246007 MS01a03.x
16	17	343	5.1	549	12	BP109970	BP109970 BP109970
17	18	343	5.1	549	12	BP109970	BP109970 BP109970
18	19	341	5.1	456	14	B02483	B02483 y86c03.t1
19	20	333.6	5.0	369	10	BS246007	BS246007 MS01a03.x
20	21	333.6	5.0	369	10	BS246007	BS246007 MS01a03.x
21	22	315	4.7	458	13	BX785297	BX785297 BX785297
22	23	308.8	4.6	600	28	AC681683	AC681683 HS_2161.A
23	24	306.8	4.6	638	10	BS480212	BS480212 BS480212
24	25	306.8	4.6	638	10	BS480212	BS480212 BS480212
25	26	306.8	4.6	638	10	BS480212	BS480212 BS480212
26	27	255.2	3.8	667	10	BS480212	BS480212 BS480212
27	28	255.2	3.8	667	10	BS480212	BS480212 BS480212
28	29	255.2	3.8	667	10	BS480212	BS480212 BS480212
29	30	255.2	3.8	667	10	BS480212	BS480212 BS480212

C 28 250.8 3.7 544 10 EC018841
 C 29 248.4 3.7 319 2 NSM070959
 C 30 248.4 3.7 1374 11 EC017002
 C 31 247.8 3.7 598 28 AQ489530
 C 32 247.8 3.7 663 2 NSM072801
 C 33 247.4 3.7 663 2 NSM072801
 C 34 246 3.7 605 14 CM434583
 C 35 246 3.7 769 29 AQ386056
 C 36 246 3.7 582 28 AQ386524
 C 37 245.4 3.7 582 28 AQ386524
 C 38 244.8 3.6 625 12 BM689011
 C 39 244.2 3.6 1643 12 BM619569
 C 40 243.2 3.6 469 28 B75932
 C 41 243.2 3.6 408 28 AQ219156
 C 42 243 3.6 469 28 B75932
 C 43 243 3.6 790 29 AQ483221
 C 44 242.2 3.6 383 10 EC019174
 C 45 242.2 3.6 383 10 EC019174

Search completed: January 7, 2004, 21:22:33
 Job time : 12396 secs

EC018841 609610570
 BK485801 Homo sapi
 EC017002 Homo sapi
 AQ489530 RNC1-11.2
 EC017002 Homo sapi
 BK482631 Homo sapi
 CM434583 UI-H-DHO-
 AQ386056 RNC11-14
 AQ386524 RNC11-14
 AQ386524 RNC11-14
 BM689011 UI-H-DFO-
 BM619569 AGSMOUNT
 B75932 RNC11-12N1
 AQ219156 HS-3259.8
 B75932 RNC11-12N1
 AQ219174 Pan trogl
 AQ483221 RNC11-14
 EC019174 Homo sapi
 EC019174 60341718